



SEQUENCE LISTING

<110> POLYMERPOULOUS, MIHAEL
LAVEDAN, CHRISTIAN
LEROY, ELISABETH
NUSSBAUM, ROBERT
JOHNSON, WILLIAM
DUVOISIN, ROGER

<120> CLONING OF A GENE MUTATION FOR PARKINSON'S DISEASE

<130> 31978-164334

<140> 09/446,628

<141> 1998-06-25

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (133)

<223> a, t, c, g, other or unknown

<220>

<221> CDS

<222> (56)..(97)

<400> 1

gctaatacagc aatttaaggc tagcttgaga cttatgtctt gaatttggtt ttgta ggc 58
Gly
1

tcc aaa acc aag gag gga gtg gtg cat ggt gtg aca aca ggtaagctcc 107
Ser Lys Thr Lys Glu Gly Val Val His Gly Val Thr Thr
5 10

attgtgctta tatcaaagat gatantaaa gtatctagt attagtgtgg cccagtatca 167

agattcctat gaaattgtaa aacaatcact gagcatctaa gaacatatc 216

<210> 2

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 2

gctaatacagc aatttaggct ag

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 3
 ctatacaaga atctacgagt c

21

<210> 4
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Glu Thr Ala Ser Pro Val Ala Leu Pro His Glu Met Glu Thr Leu
 1 5 10 15
 Tyr Ser Gly Leu Tyr Leu Glu Ser Glu Arg Leu Tyr Ser Ala Leu Ala
 20 25 30
 Leu Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Ala Leu
 35 40 45
 Ala Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu
 50 55 60
 Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Ala Leu Ala Gly Leu
 65 70 75 80
 Ala Leu Ala Ala Leu Ala Gly Leu Tyr Leu Tyr Ser Thr His Arg Leu
 85 90 95
 Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Leu Glu Thr Tyr Arg Val
 100 105 110
 Ala Leu Gly Leu Tyr Ser Glu Arg Leu Tyr Ser Thr His Arg Leu Tyr
 115 120 125
 Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu His Ile Ser Gly
 130 135 140
 Leu Tyr Val Ala Leu Ala Leu Ala Thr His Arg Val Ala Leu Ala Leu
 145 150 155 160
 Ala Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly Leu
 165 170 175
 Asn Val Ala Leu Thr His Arg Ala Ser Asn Val Ala Leu Gly Leu Tyr
 180 185 190
 Gly Leu Tyr Ala Leu Ala Val Ala Leu Val Ala Leu Thr His Arg Gly
 195 200 205

Leu Tyr Val Ala Leu Thr His Arg Ala Leu Ala Val Ala Leu Ala Leu
210 215 220

Ala Gly Leu Asn Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu Gly
225 230 235 240

Leu Tyr Ala Leu Ala Gly Leu Tyr Ser Glu Arg Ile Leu Glu Ala Leu
245 250 255

Ala Ala Leu Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Pro His Glu
260 265 270

Val Ala Leu Leu Tyr Ser Leu Tyr Ser Ala Ser Pro Gly Leu Asn Leu
275 280 285

Glu Gly Leu Tyr Leu Tyr Ser Ala Ser Asn Gly Leu Gly Leu Gly Leu
290 295 300

Tyr Ala Leu Ala Pro Arg Gly Leu Asn Gly Leu Gly Leu Tyr Ile Leu
305 310 315 320

Glu Leu Glu Gly Leu Ala Ser Pro Met Glu Thr Pro Arg Val Ala Leu
325 330 335

Ala Ser Pro Pro Arg Ala Ser Pro Ala Ser Asn Gly Leu Ala Leu Ala
340 345 350

Thr Tyr Arg Gly Leu Met Glu Thr Pro Arg Ser Glu Arg Gly Leu Gly
355 360 365

Leu Gly Leu Tyr Thr Tyr Arg Gly Leu Asn Ala Ser Pro Thr Tyr Arg
370 375 380

Gly Leu Pro Arg Gly Leu Ala Leu Ala
385 390

<210> 5

<211> 394

<212> PRT

<213> Rattus norvegicus

<400> 5

Met Glu Thr Ala Ser Pro Val Ala Leu Pro His Glu Met Glu Thr Leu
1 5 10 15

Tyr Ser Gly Leu Tyr Leu Glu Ser Glu Arg Leu Tyr Ser Ala Leu Ala
20 25 30

Leu Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Ala Leu
35 40 45

Ala Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu
50 55 60

Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Ala Leu Ala Gly Leu
65 70 75 80

Ala Leu Ala Ala Leu Ala Gly Leu Tyr Leu Tyr Ser Thr His Arg Leu
 85 90 95

Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Leu Glu Thr Tyr Arg Val
 100 105 110

Ala Leu Gly Leu Tyr Ser Glu Arg Leu Tyr Ser Thr His Arg Leu Tyr
 115 120 125

Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu His Ile Ser Gly
 130 135 140

Leu Tyr Val Ala Leu Thr His Arg Thr His Arg Val Ala Leu Ala Leu
 145 150 155 160

Ala Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly Leu
 165 170 175

Asn Val Ala Leu Thr His Arg Ala Ser Asn Val Ala Leu Gly Leu Tyr
 180 185 190

Gly Leu Tyr Ala Leu Ala Val Ala Leu Val Ala Leu Thr His Arg Gly
 195 200 205

Leu Tyr Val Ala Leu Thr His Arg Ala Leu Ala Val Ala Leu Ala Leu
 210 215 220

Ala Gly Leu Asn Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu Gly
 225 230 235 240

Leu Tyr Ala Leu Ala Gly Leu Tyr Ala Ser Asn Ile Leu Glu Ala Leu
 245 250 255

Ala Ala Leu Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Pro His Glu
 260 265 270

Val Ala Leu Leu Tyr Ser Leu Tyr Ser Ala Ser Pro Gly Leu Asn Met
 275 280 285

Glu Thr Gly Leu Tyr Leu Tyr Ser Gly Leu Tyr Gly Leu Gly Leu Gly
 290 295 300

Leu Tyr Thr Tyr Arg Pro Arg Gly Leu Asn Gly Leu Gly Leu Tyr Ile
 305 310 315 320

Leu Glu Leu Glu Gly Leu Ala Ser Pro Met Glu Thr Pro Arg Val Ala
 325 330 335

Leu Ala Ser Pro Pro Arg Ser Glu Arg Ser Glu Arg Gly Leu Ala Leu
 340 345 350

Ala Thr Tyr Arg Gly Leu Met Glu Thr Pro Arg Ser Glu Arg Gly Leu
 355 360 365

Gly Leu Gly Leu Tyr Thr Tyr Arg Gly Leu Asn Ala Ser Pro Thr Tyr
 370 375 380

Arg Gly Leu Pro Arg Gly Leu Ala Leu Ala
385 390

<210> 6
<211> 362
<212> PRT
<213> Bos taurus

<400> 6
Met Glu Thr Ala Ser Pro Val Ala Leu Pro His Glu Met Glu Thr Leu
1 5 10 15
Tyr Ser Gly Leu Tyr Leu Glu Ser Glu Arg Met Glu Thr Ala Leu Ala
20 25 30
Leu Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Ala Leu
35 40 45
Ala Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu
50 55 60
Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Thr His Arg Gly Leu
65 70 75 80
Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr
85 90 95
Ser Gly Leu Gly Leu Tyr Val Ala Leu Leu Glu Thr Tyr Arg Val Ala
100 105 110
Leu Gly Leu Tyr Ser Glu Arg Leu Tyr Ser Thr His Arg Leu Tyr Ser
115 120 125
Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Gly Leu Asn Gly Leu
130 135 140
Tyr Val Ala Leu Ala Leu Ala Ser Glu Arg Val Ala Leu Ala Leu Ala
145 150 155 160
Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly Leu Asn
165 170 175
Ala Leu Ala Ser Glu Arg His Ile Ser Leu Glu Gly Leu Tyr Gly Leu
180 185 190
Tyr Ala Leu Ala Val Ala Leu Pro His Glu Ser Glu Arg Gly Leu Tyr
195 200 205
Ala Leu Ala Gly Leu Tyr Ala Ser Asn Ile Leu Glu Ala Leu Ala Ala
210 215 220
Leu Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Leu Glu Val Ala Leu
225 230 235 240
Leu Tyr Ser Leu Tyr Ser Gly Leu Gly Leu Pro His Glu Pro Arg Thr
245 250 255

His Arg Ala Ser Pro Leu Glu Leu Tyr Ser Pro Arg Gly Leu Gly Leu
 260 265 270

Val Ala Leu Ala Leu Ala Gly Leu Asn Gly Leu Ala Leu Ala Ala Leu
 275 280 285

Ala Gly Leu Gly Leu Pro Arg Leu Glu Ile Leu Glu Gly Leu Pro Arg
 290 295 300

Leu Glu Met Glu Thr Gly Leu Pro Arg Gly Leu Gly Leu Tyr Gly Leu
 305 310 315 320

Ser Glu Arg Thr Tyr Arg Gly Leu Gly Leu Gly Leu Asn Pro Arg Gly
 325 330 335

Leu Asn Gly Leu Gly Leu Thr Tyr Arg Gly Leu Asn Gly Leu Thr Tyr
 340 345 350

Arg Gly Leu Pro Arg Gly Leu Ala Leu Ala
 355 360

<210> 7

<211> 399

<212> PRT

<213> Serinus canaria

<400> 7

Met Glu Thr Ala Ser Pro Val Ala Leu Pro His Glu Met Glu Thr Leu
 1 5 10 15

Tyr Ser Gly Leu Tyr Leu Glu Ser Glu Arg Leu Tyr Ser Ala Leu Ala
 20 25 30

Leu Tyr Ser Gly Leu Val Ala Leu Val Ala Leu Ala Leu Ala Ala Leu
 35 40 45

Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly
 50 55 60

Leu Asn Gly Leu Tyr Val Ala Leu Ala Leu Ala Gly Leu Ala Leu Ala
 65 70 75 80

Ala Leu Ala Gly Leu Tyr Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly
 85 90 95

Leu Gly Leu Tyr Val Ala Leu Leu Glu Thr Tyr Arg Val Ala Leu Gly
 100 105 110

Leu Tyr Ser Glu Arg Ala Arg Gly Thr His Arg Leu Tyr Ser Gly Leu
 115 120 125

Gly Leu Tyr Val Ala Leu Val Ala Leu His Ile Ser Gly Leu Tyr Val
 130 135 140

Ala Leu Thr His Arg Thr His Arg Val Ala Leu Ala Leu Ala Gly Leu
 145 150 155 160

Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly Leu Asn Val Ala
165 170 175

Leu Ser Glu Arg Ala Ser Asn Val Ala Leu Gly Leu Tyr Gly Leu Tyr
180 185 190

Ala Leu Ala Val Ala Leu Val Ala Leu Thr His Arg Gly Leu Tyr Val
195 200 205

Ala Leu Thr His Arg Ala Leu Ala Val Ala Leu Ala Leu Ala Gly Leu
210 215 220

Asn Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu Gly Leu Tyr Ala
225 230 235 240

Leu Ala Gly Leu Tyr Ala Ser Asn Ile Leu Glu Ala Leu Ala Ala Leu
245 250 255

Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Leu Glu Val Ala Leu Leu
260 265 270

Tyr Ser Leu Tyr Ser Ala Ser Pro Gly Leu Asn Leu Glu Ala Leu Ala
275 280 285

Leu Tyr Ser Gly Leu Asn Ala Ser Asn Gly Leu Gly Leu Gly Leu Tyr
290 295 300

Pro His Glu Leu Glu Gly Leu Asn Gly Leu Gly Leu Tyr Met Glu Thr
305 310 315 320

Val Ala Leu Ala Ser Asn Ala Ser Asn Thr His Arg Gly Leu Tyr Ala
325 330 335

Leu Ala Ala Leu Ala Val Ala Leu Ala Ser Pro Pro Arg Ala Ser Pro
340 345 350

Ala Ser Asn Gly Leu Ala Leu Ala Thr Tyr Arg Gly Leu Met Glu Thr
355 360 365

Pro Arg Pro Arg Gly Leu Gly Leu Gly Leu Thr Tyr Arg Gly Leu Asn
370 375 380

Ala Ser Pro Thr Tyr Arg Gly Leu Pro Arg Gly Leu Ala Leu Ala
385 390 395

<210> 8

<211> 405

<212> PRT

<213> Torpedo californica

<400> 8

Met Glu Thr Ala Ser Pro Val Ala Leu Leu Glu Leu Tyr Ser Leu Tyr
1 5 10 15

Ser Gly Leu Tyr Pro His Glu Ser Glu Arg Pro His Glu Ala Leu Ala
20 25 30

Leu Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Ala Leu
 35 40 45
 Ala Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu
 50 55 60
 Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Gly Leu Asn Ala Ser
 65 70 75 80
 Pro Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu
 85 90 95
 Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Gly Leu Asn Ala Ser
 100 105 110
 Pro Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu
 115 120 125
 Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Met Glu Thr Thr Tyr Arg
 130 135 140
 Val Ala Leu Gly Leu Tyr Thr His Arg Leu Tyr Ser Thr His Arg Leu
 145 150 155 160
 Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Gly Leu Asn
 165 170 175
 Ser Glu Arg Val Ala Leu Ala Ser Asn Thr His Arg Val Ala Leu Thr
 180 185 190
 His Arg Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly
 195 200 205
 Leu Asn Ala Leu Ala Ala Ser Asn Val Ala Leu Val Ala Leu Gly Leu
 210 215 220
 Tyr Gly Leu Tyr Ala Leu Ala Val Ala Leu Val Ala Leu Ala Leu Ala
 225 230 235 240
 Gly Leu Tyr Val Ala Leu Ala Ser Asn Thr His Arg Val Ala Leu Ala
 245 250 255
 Leu Ala Ser Glu Arg Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu
 260 265 270
 Gly Leu Tyr Val Ala Leu Gly Leu Ala Ser Asn Val Ala Leu Ala Leu
 275 280 285
 Ala Ala Leu Ala Ala Leu Ala Ser Glu Arg Gly Leu Tyr Val Ala Leu
 290 295 300
 Val Ala Leu Leu Tyr Ser Leu Glu Ala Ser Pro Gly Leu His Ile Ser
 305 310 315 320
 Gly Leu Tyr Ala Arg Gly Gly Leu Ile Leu Glu Pro Arg Ala Leu Ala
 325 330 335

Gly Leu Gly Leu Asn Val Ala Leu Ala Leu Ala Gly Leu Gly Leu Tyr
 340 345 350
 Leu Tyr Ser Gly Leu Asn Thr His Arg Thr His Arg Gly Leu Asn Gly
 355 360 365
 Leu Pro Arg Leu Glu Val Ala Leu Gly Leu Ala Leu Ala Thr His Arg
 370 375 380
 Gly Leu Ala Leu Ala Thr His Arg Gly Leu Gly Leu Thr His Arg Gly
 385 390 395 400
 Leu Tyr Leu Tyr Ser
 405

<210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
 acgacagtgt gtgtaaagg

19

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 10
 aacatctgtc agcagatctc

20

<210> 11
 <211> 2804
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (83)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (89)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base

<222> (138)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (140)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (220)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (247)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (456)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (463)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (553)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (555)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (570)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (577)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (580)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (602)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (612)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (671)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (690)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (695)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (697)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (704)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (711)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (869)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (1174)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (1286)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (1720)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base

<222> (1806)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1845)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (2002)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (2004)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (2029)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (2042)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (2051)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (2122)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (2152)
 <223> a, t, c, g, other or unknown

<400> 11
 ccgccgcagc cgccgctcca tccccagccc cggccccgca tccggtttgg aagggggctg 60
 caagtttgca agggggcccgg ganaaaaaanc gagcagtggc ccttcccgcg tccccagggg 120
 ttcaagggac gctaggantn tccgcggccc tggaggttcg cactggggag tggggtgaga 180
 tggggggaaa gcgggagggg gctcagggtc cagaagggcn ccgcgggtctc gggagtaggg 240
 gggcatntgc gtcccgcggg aggggctggg gtgagagtgc ggggccagtg caccggtgcc 300
 cgtgtatcgc cctccccagg ccgccaggat ggacgtgttc atgaagggcc tgtccatggc 360
 caaggagggc gttgtggcag ccgcggagaa aaccaagcag ggggtcaccg aggcggcgga 420
 gaagaccaag gagggcgtec tctacgtcgg tgggcngggg gcnggggttc tggggctgca 480
 gggctggggg tccccctaca gtgtggagct ggggcccggg cccggggagg ggggttctgg 540
 gcaagataat atnancagc agatggggcn aggtcancan gggtcataag ggacataccc 600
 ancccataga ancctgggtc tgtatccgga aatggggaca cggggcgggc tgatgaggtg 660
 gggggctcca nctgaaaggc cagggaccan tgcantnata aaancacaca nctcctttt 720
 tcttatcttt tttaccatta ttaatagtta tctggtgttg aacactttct gtatgccaag 780
 tactgggtaa aatgtcataa catccatttc ctcatgtaat gttccgccc attctacagg 840

```

taagggaaac tggggttccc attggtagnt aaatttttagg ttcagaaagg cttgaattga 900
atgtcagttc agccaatttc ttagtggtgg aacccaaactg agttccatcc gtgaaacggg 960
gacaataaca gcaccccgctt cccagggctg gggaaaaagtg aagtgtagcg gggcaggcag 1000
aggacttgac acagcactgg cctcagcca acatccacta gaggggtggg gtatcgcatc 1080
aggtgggaga gaaatgcaac ccttgccagc agaggtgtgg ggcccagtgc agtgataaga 1140
cggggggttaa catgggggtg caggtttagt gatntgggga cccaaaggag cagtgcaggg 1200
gccaggatgc ccaactctgt atcaccatgc tgtgctggag ttctgttcc ctcagcgag 1260
agtccttaaa tgtgcgcgtt ttctnccct gcaggaaagca agaccgcaga aggtgtggta 1320
caaggtgtgg cttcaggtac tagcccagcc ctggcaccag cccttctctc amttaggcgg 1380
atgatctggc cgggaaccag agggcggggg cgggggagac tcccaaggct tctgcgggaa 1440
tgctccgtgg ggagggcagg ccttgggata ctacaaggca gggcatcggg gtttccccct 1500
gggtcccaaa ccccttctc aacccccctc ctgctccagt ggctgaaaaa accaaggaa 1560
aggcctcaca tctgggagga gctgtgttct ctggggcagg gaacatcgca gcagccacag 1620
gactggtgaa gagggaggaa ttccctactg atctgaagg aagcgatcct tctgaccgc 1680
acatgcaggc aaacacacac acacacacac acacacacacn ggcacacaaa taaacctgtc 1740
accatccccg cccccctaat cctgccacca gcttggaaaca caagccactt tgccctccat 1800
cctgcnngcc cgtgctagac tcagctcaga atgcattctga ataanggcgt gcatgggtgt 1860
gacgtccccg gtgatgggga cccagacctg gctgtctgcg tgtatcctgc ttgccagcgt 1920
gacccatag acttctggcc acgtctgcat gtgtcaatga ttgttcattc atttcttttc 1980
attcaacaaa tatccatgcc ananccagcc ctgtccttga gcttccagnt ccctttcagc 2040
cnaggggagc ntgaggggta tttttggggg cccgatgccc agcacagagc ctgacacaaa 2100
ggatgaggca taagctggtg antgagtatc caaatggtgg aagtgtggag gntgccaggc 2160
attgggggag cggcgtggag agccagctcc ccaatccatg ctgccacttc aactgtgatt 2220
cgggggaatt tcccccttca cctccatccc acttccaagg cactccaaat aaataactga 2280
attagaaatt atccttgttt tgccaaccca cctagcctt cccactcca acccacccaa 2340
agcttaccac tgtgggaatt tggggggcat cctggctgtc ctacagagtc ctgacctttt 2400
ctgcccacag ccagaggaag tggcccagga agctgctgaa gaaccactga ttgagcccc 2460
gatggagcca gaaggggaga gttatgagga cccaccccag gaggaatata aggagatga 2520
gccagggcg tagggggcca ggagagcccc caccagcagc acaattctgt cctgtccct 2580
gccccgcccc ccagagccag ggctgtcctt agactccttc tccccaatca cgagatcttc 2640
cttccgctct gaggcaaccc cctcggagcc tgtgttagtg tctgtccatc tgtctgtcct 2700
acccgccccg gtccaacccc ggggcattga cagggccagg gttgcggtcg cggctgggag 2760
cctcgccccct ccagtgttgc ctctcccat ccagcgtctg cgcg 2804

```

<210> 12

<211> 223

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (94)

<223> a, t, c, g, other or unknown

<400> 12

```

agggagatcc agctccgtcc tgctgcagc agcacaaccc tgcacaccca ccatggatgt 60
cttcaagaag ggcttctcca tcgccaagga gggngtggtg ggtgcgggtg aaaagaccaa 120
gcagggggtg acggaagcag ctgagaagac caaggagggg gtcattgtat tgggattaca 180
tttttttttt aaagaaagaa taaattaatt gtgattaaag ttg 223

```

<210> 13

<211> 677

<212> DNA

<213> Homo sapiens

<220>
<221> modified_base
<222> (7)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (28)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (34)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (36)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (51)..(52)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (69)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (74)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (80)..(81)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (86)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (90)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (94)..(95)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base

<222> (98)
<223> a, t, c, g, other or unknown

<210>
<221> modified_base
<222> (100)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (109)..(110)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (112)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (114)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (117)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (137)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (150)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (153)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (156)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (162)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (168)
<223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (175)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (194)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (202)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (210)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (228)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (232)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (237)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (246)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (251)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (253)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (262)
 <223> a, t, c, g, other or unknown

<400> 13
 ttttttnagg ggggaaaaca gggaatanaa aaanangggg ggggggttttt nngggggggg 60
 ggggaaaang gttnngggggn naaccnaaan aaannccnan gggggggggn antnaanttt 120


```

tgggaaccca aagcccnagg aggatttttn gtnaanaacg tnacctcnag tgggnecgagg 180
aagaccaagg aaangcccaa cncggttgan cgaggctgtg gtgaacancg tncaacnctg 240
tgcccnccaa nancgtggag gngggggaga acatcscggg cacctccggg gtggtgcgcm 300
aggaggactt gaggccatct kccccccmac aggagggtgt ggcateccmaa garaaagagg 360
aagtggcaga ggaggcccag agtgggggar actagagggc tacaggccag cgtggatgac 420
ctgaagagcg ctctcttgcc ttggacacca tccccctcta gcacaaggag tgcccgctt 480
gagtgcacatg cggctgcccc cgctctgccc ctctcttccc tggccaccct tgacctgtcc 540
acctgtgctg ctgcaccaac ctcaactgccc tccctcgccc ccaccaccc tctgggtcctt 600
ctgacccccc ttatgctgct gtgaattttt tttttaaatg attccaaata aaacttgagc 660
ccactccaaa aaaaaaaa                                     677

```

<210> 14

<211> 1181

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (130)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (140)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (172)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (193)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (329)..(330)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (902)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (965)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (1015)

<223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1159)
 <223> a, t, c, g, other or unknown

<400> 14
 aatttcagcg atgcgagggc aaagcgctct cggcgggtgcg gtgtgagcca cctcccggcg 60
 ctgcctgtct cctccagcag ctccccaagg gataggctct gcccttggtg gtcgaccctc 120
 aggcctcgn tctcccaggn cgactctgac gaggggtagg ggggtggccc cnggaggacc 180
 cagaggaaaag gcngggacaa gaagggaggg gaaggggaaa gaggaagagg catcatccct 240
 agcccaaccg ctcccgatct ccacaagagt gctcgtgacc ctaaaacttaa cgtgaggcgc 300
 aaaagcgccc caaccttttc ccgccttggn ccaggcaggc ggctggagtt gatggctcac 360
 cccgcgcccc ctgccccatc cccatccgag atagggacga ggagcacgct gcagggaaaag 420
 cagcgagcgc cgggagaggg gcgggcagaa gcgctgacaa atcagcgggtg ggggcggaga 480
 gccgaggaga aggagaagga ggaggactag gaggaggagg acggcgacga ccagaagggg 540
 cccaagagag ggggagagcg accgagcgcc gcgacgcgaa gtgagggtgcg tgcggggtca 600
 gcgcagaccc cggcccggcc cctcctgaga gcgtcctggg cgctccctca cgcttgctc 660
 tcaagccttc tgccctttcca cctcctgtag cggagaactg ggagtggcca ttcgacgaca 720
 gggttagcggg tttgcctccc actccccag cctcgcgtcg ccggctcaca gcggcctcct 780
 ctggggacag tcccccccg gtgcccctcc gcccttcctg tgcgctcctt ttccttcttc 840
 tttcctatta aatattatct gggaattgtt taaatttttt ttttaaaaaa agagagaggc 900
 gnggaggagt cggagtgtgt gagaagcaga gggactcagg taagtacctg tggatctaaa 960
 cggngtctt ttggaaatcc tggagaacgc cggatggaga cgaatggctg tgggnaccgg 1020
 gagggggtgg tgctgccatg aggaccgctg ggccaggctc ctgggagggt agtacttgct 1080
 ctttggggag ctaaggaaaag agacttgacc tggctttcgt cctgcttctg atattccctt 1140
 ctccacaagg gctgagagnt taggctgctt ctccgggatc c 1181

<210> 15
 <211> 536
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (422)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (481)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (490)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (525)
 <223> a, t, c, g, other or unknown

<400> 15
 cttaaaagag tctcacactt tggagggttt ctcatgattt ttcagtgttt tttgtttatt 60
 tttccccgaa agttctcatt caaagtgtat tttatgtttt ccagtgtggt gtaaagaaat 120
 tcattagcca tggatgtatt catgaaagga ctttcaaagg ccaaggaggg agttgtggct 180
 gctgctgaga aaaccaaaca ggggtgtggc gaagcagcag gaaagacaaa agagggtgtt 240

```

ctctatgtag gtaggtaaac cccaaatgtc agtttggtgc ttgttcatga gtgatgggtt 300
aggataacaa tactctaaat gctggtagtt ctctctcttg attcattttt gcacatttgc 360
ttgtcaaaaa ggtggactga gtcagaggta tgtgtaggta ggtgaatgtg aacgtgtgta 420
tntgagctaa tagtaaaaaat gcgactgttt gcttttcaga tttttaattt tgcctaatat 480
ntatgacttn ttaaaatgaa tgtttctgta ctacataatt ctatntcaga gacagt 536

```

<210> 16

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (214)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (476)

<223> a, t, c, g, other or unknown

<400> 16

```

ctgcaggcca acggatctgt ctctagtgtt gtacttttaa agcttctaca gttctgaatt 60
caaaattatc ttctcactgg gccccgggtg tatctcattc ttttttctcc tctgtaagtt 120
gacatgtgat gtgggaacaa aggggataaa gtcattattt tgtgctaaaa tcgtaattgg 180
agaggacctc ctgttagctg ggctttcttc tatntattgt ggtggttagg agttccttct 240
tctagtttta ggatatatat atatatTTTT tctttccctg aagatataat aatatatata 300
cttctgaaga ttgagatttt taaattagtt gtattgaaaa ctagctaata agcaatttaa 360
ggctagcttg agacttatgt cttgaatttg tttttgtagg ctccaaaacc aaggagggag 420
tggtgcatgg tgtggcaaca ggtaagctcc attgtgctta tatcaaagat gatatntaaa 480
gtatctagtg attagtgtgg ccagtatcca agattcctat tgaaattgta aaacaatcac 540
tgagcatcta agaacatata agtcttattg aaactgaatt ctttataaag tattttttaa 600
taggtaaata ttgattataa ataaaaaata tacttgccaa gaataatgag 650

```

<210> 17

<211> 504

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (117)

<223> a, t, c, g, other or unknown

<400> 17

```

atatcttagc caagattcaa tgtttggttg aaccacactc acttgacatc ttggtggctt 60
ttgtttcttc tgaccactca gttatctatg gcatgtgtag atacagggtg atggaancga 120
tggttagtgg aagtggaaatg attttaagtc actgttatcc taccaccctt taatctgttg 180
ttgtctttta tttgtaccag tggctgagaa gaccaaaagag caagtgacaa atgttgaggg 240
agcagtgggtg acgggtgtga cagcagtagc ccagaagaca gtggagggag caggagagcat 300
tgcagcagcc actggctttg tcaaaaagga ccagttgggc aaggtatggc tgtgtacgtt 360
ttgtgttaca ttataagct ggtgagatta cggttcattt tcatgtgaag cctggaggca 420
ggagcaagat acttactgtg gggaacggct acctgaccct ccccttgtga aaaagtgtca 480
cctttatatt ggtcttgctt gttt 504

```

<210> 18
 <211> 726
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (553)
 <223> a, t, c, g, other or unknown

<400> 18
 aaaagttttac atacttttgag gttgataaacc catgttgccg caatgtttcc ccggaggcat 60
 tgtggagttt agaatgccag tagtaatat aagggtgtgcc attttcaaga tccgtggcca 120
 acatccctat atgtaagatt ttccaaaac atgggtctga tttttaaaag tgaaaaatgc 180
 tacttcatca tgttcttttt gtgcttctta ctttaaatat tagaatgaag aaggagcccc 240
 acaggaagga attctggaag atatgcctgt ggatcctgac aatgaggctt atgaaatgcc 300
 ttctgaggta ggagtccaag ctgaatcttt ctaacaagac agtaccaaaa acctgtcatt 360
 gtcacatttc tctttcatta gtgcttagtg agaatcattt gctctctaca tgctcattag 420
 tggacaactt gcaagttaag aatagttttt acatttttaa agggtcctta aaaaaaaaga 480
 ggaggaggaa gatgaagaag aggaagaaaag gatgtaaaaag aaatcatatg tagtccacat 540
 agcttaatat acntactact tgaccttcta caggaaaaagc tttactaacc cctgcattag 600
 agaatatatt tttttgcaaa aacattgatt gtaaatttta gtgtaaagtg gggagccatt 660
 tctatctca ttggctgtcc agtgcctgat cgtaattgaa acttatacta acagtgtgtg 720
 ctgtct 726

<210> 19
 <211> 1596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (415)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (486)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (585)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1119)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1419)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base

<222> (1503)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1549)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1554)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1561)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1581)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1589)
 <223> a, t, c, g, other or unknown

<400> 19
 ttttgatttt tctaataatta ggaagggtat caagactacg aacctgaagc ctaagaaata 60
 tctttgctcc cagtttcttg agatctgctg acagatgttc catcctgtac aagtgtcag 120
 ttccaatgtg cccagtcattg acatttctca aagtttttac agtgtatctc gaagtcttcc 180
 atcagcagtg attgaagcat ctgtacctgc cccactcag catttcggtg cttccctttc 240
 actgaagtga atacatggta gcagggtctt tgtgtgctgt ggattttgtg gcttcaatct 300
 acgatgttaa aacaaattaa aaacacctaa gtgactacca cttatttcta aatcctcact 360
 attttttgtg tgctgttgtt cagaagttgt tagtgatttg ctatcatata ttatnagatt 420
 tttagggtgc ttttaattgat actgtctaag aataatgacg tattgtgaaa tttgttaata 480
 tataatnatac ttaaaaaatat gtgagcatga aactatgcac ctataatact aaatatgaaa 540
 ttttaccatt ttgcgatgtg ttttattcac ttgtgtttgt atatnaatgg tgagaattaa 600
 aataaaacgt tatctcattg caaaaatatt ttatttttat cccatctcac ttttaataata 660
 aaaatcatgc ttataagcaa catgaattaa gaactgacac aaaggacaaa aatataaagt 720
 tattaatagc catttgaaga aggaggaatt ttagaagagg tagagaaaat ggaacattaa 780
 ccctacactc ggaattccct gaagcaacac tgccagaagt gtgttttggg atgcactggg 840
 tccttaagtg gctgtgatta attattgaaa gtgggtgtgt gaagacccca actactattg 900
 tagagtgggc tatttctccc ttcaatcctg tcaatgtttg ctttacgtat tttggggaac 960
 tgttgtttga tgtgtatgtg tttataattg ttatacattt ttaattgagc cttttattaa 1020
 catatatgtt tatttttgtc tcgaaataat tttttagtta aaatctattt tgtctgatat 1080
 tgggtgtgaat gctgtacctt tctgacaata aataatatnc gaccatgaat aaaaaaaaaa 1140
 aaaaagtggg ttcccgggaa ctaagcagtg tagaagatga ttttgactac accctcctta 1200
 gagagccata agacacatta gcacatatta gcacattcaa ggctctgaga gaatgtgggt 1260
 aactttgttt aactcagcat tctcactttt ttttttttaa tcatcagaaa ttctctctct 1320
 ctctctcttt ttctctctgt ctcttttttt tttttttttt ttttacagga aatgccttta 1380
 aacatcgttg ggaactacca gagtcacctt aaaggaggna tcaattctct aggactggat 1440
 aaaaatttca tgggcctcct ttaaaatgtt gcccaaatat atggaattct aggggttttt 1500
 centagggggg aagggttttt tctcttttctn ggggaggatc cttttaacnc cccngggggg 1560
 ngccccgaaa ataaacttgg ngggggggna aaactt 1596

<210> 20
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 atgtcttcaa gaagggttc

20

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
 ccttggtctt ctacgtgct

20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
 agcgtggatg acctgaagag

20

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 agcacaggtg gacaggccaa g

21

<210> 24
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 24
 gatatgttct tagatgctca g

21

<210> 25

<211> 14

<212> PRT

<213> Homo sapiens

<400> 25

Gly Ser Lys Thr Lys Glu Gly Val Val His Gly Val Thr Thr

1

5

10